

## **Supplemental Material**

# **Interaction between Arsenic Exposure from Drinking Water and Genetic Polymorphisms on Cardiovascular Disease in Bangladesh: A Prospective Case-Cohort Study**

Fen Wu, Farzana Jasmine, Muhammad G. Kibriya, Mengling Liu, Xin Cheng, Faruque Parvez, Tariqul Islam, Alauddin Ahmed, Muhammad Rakibuz-Zaman, Jieying Jiang, Shantanu Roy, Rachelle Paul-Brutus, Vesna Slavkovich, Tariqul Islam, Diane Levy, Tyler J. VanderWeele, Brandon L. Pierce, Joseph H. Graziano, Habibul Ahsan, and Yu Chen

**Table S1.** Detailed information on the selected SNPs.

db SNP ID <sup>a</sup>	SNP position	Alleles	Role [amino acid change]	Prior studies min MAF <sup>b</sup>	Prior studies max MAF <sup>b</sup>	Present study minor allele	Present study MAF
<b>APOE 19q13.32</b>							
rs1081101	45408077	C/T	Promoter	-	-	T	0.000
rs12982192	45411259	C/T	Intron (boundary)	-	-	C	0.000
<b>rs405509</b>	45408836	A/C	Promoter	0.204	0.487	C	0.463
<b>rs429358</b>	45411941	C/T	Coding exon [C130R]	0.000	0.018	C	0.103
rs434132	45407720	C/G	Promoter	-	-	C	0.001
rs435380	45407118	C/T	Promoter	-	-	T	0.008
rs446037	45407437	A/C	Promoter	-	-	A	0.000
rs7256173	45407655	C/T	Promoter	-	-	T	0.020
<b>rs7259620</b>	45407788	A/G	Promoter	-	-	A	0.405
rs769445	45408312	C/T	Promoter	-	-	T	0.002
rs769451	45410911	G/T	Intron	0.007	0.014	G	0.001
rs769452	45411110	C/T	Coding exon [L46P]	-	-	C	0.000
rs877973	45409283	G/T	Intron	-	-	T	0.000
<b>AS3MT 10q24.32</b>							
<b>rs1046778</b>	104661484	C/T	3' UTR	0.213	0.488	C	0.348
rs10509760	104634107	C/T	Intron	0.007	0.160	C	0.043
rs10509761	104632769	A/G	Intron (boundary)	0.000	0.175	G	0.000
<b>rs10748835</b>	104660256	A/G	Intron (boundary)	0.306	0.494	A	0.439
<b>rs10748839</b>	104953547	C/T	Promoter	0.324	0.488	C	0.435
<b>rs10786719</b>	104637992	A/G	Intron	0.306	0.494	G	0.438
<b>rs10883790</b>	104640955	A/C	Intron	0.121	0.304	C	0.250
<b>rs10883795</b>	104654577	C/T	Intron	0.191	0.432	C	0.348
<b>rs11191438</b>	104637864	C/G	Intron	0.306	0.494	C	0.436
<b>rs11191439</b>	104638723	C/T	Coding exon	0.007	0.149	C	0.054
<b>rs11191442</b>	104643596	A/T	Intron	0.146	0.273	A	0.251
<b>rs11191454</b>	104660004	A/G	Intron	0.000	0.305	G	0.172
<b>rs11191527</b>	104795134	C/T	Intron	0.061	0.189	T	0.158
rs11191659	105101701	C/T	Intron	0.005	0.169	T	0.044
<b>rs12573221</b>	104849144	A/C	3' UTR	0.012	0.108	C	0.121
<b>rs12774047</b>	104639738	A/G	Intron	0.048	0.163	A	0.156
rs17115203	104639969	C/T	Intron	0.000	0.093	C	0.002
<b>rs3740390</b>	104638480	A/G	Intron	0.019	0.293	A	0.175
<b>rs3740392</b>	104636855	A/G	Intron (boundary)	0.145	0.331	G	0.251
<b>rs3740393</b>	104636655	C/G	Intron (boundary)	0.099	0.293	C	0.189
rs3740394	104634474	C/T	Intron (boundary)	0.007	0.160	C	0.044
<b>rs4290163</b>	104610926	G/T	Promoter	0.255	0.488	T	0.422
<b>rs4917996</b>	104925829	A/C	Intron	0.324	0.494	C	0.447
<b>rs4919690</b>	104616500	C/T	Intron	0.078	0.292	C	0.110
<b>rs4919694</b>	104698978	C/T	Intron	0.053	0.149	C	0.090
<b>rs7085854</b>	104650251	C/T	Intron (boundary)	0.067	0.234	C	0.175
<b>rs7096169</b>	104618695	A/G	Intron	0.292	0.476	G	0.292
<b>rs7100709</b>	104649729	A/C	Intron	0.191	0.432	C	0.347
rs7907785	104641035	A/G	Intron	0.000	0.139	G	0.000
<b>rs9527</b>	104623578	A/G	3' UTR	0.073	0.292	A	0.075
<b>CBS 21q22.3</b>							
<b>rs1005585</b>	44477033	A/G	Intron (boundary)	-	-	G	0.078
<b>rs1051319</b>	44473867	C/G	3' UTR	0.068	0.389	G	0.111
<b>rs11203172</b>	44480115	G/T	Intron	0.000	0.185	T	0.053
<b>rs11700748</b>	44473062	C/T	Downstream	0.136	0.500	T	0.389
rs11701048	44491425	C/T	Intron	0.000	0.208	T	0.048
rs11910385	44491109	G/T	Intron	-	-	G	0.041
rs12613	44473691	A/G	3' UTR	-	-	A	0.035
rs13046443	44477738	C/T	Intron	-	-	T	0.000
<b>rs1789953</b>	44482936	C/T	Intron	0.043	0.277	T	0.238
rs2014564	44481169	A/G	Intron	-	-	A	0.478
<b>rs2124459</b>	44475714	C/T	Intron	0.223	0.464	C	0.411
rs2124461	44475796	C/T	Intron	-	-	T	0.474
rs2298760	44486211	A/C	Intron	-	-	A	0.000
<b>rs234701</b>	44476759	A/G	Intron	-	-	A	0.093

db SNP ID <sup>a</sup>	SNP position	Alleles	Role [amino acid change]	Prior studies min MAF <sup>b</sup>	Prior studies max MAF <sup>b</sup>	Present study minor allele	Present study MAF
rs234704	44480283	A/G	Intron	-	-	A	0.206
<b>rs234705</b>	44483772	C/T	Intron	0.022	0.436	T	0.219
<b>rs234706</b>	44485350	A/G	Coding exon [Y233Y]	0.014	0.351	A	0.209
<b>rs234709</b>	44486964	C/T	Intron	0.435	0.435	T	0.307
<b>rs234713</b>	44487891	A/G	Intron	-	-	A	0.203
<b>rs234715</b>	44488395	G/T	Intron	0.023	0.236	T	0.165
<b>rs2849727</b>	44483453	C/T	Intron	-	-	T	0.339
<b>rs2851391</b>	44487404	C/T	Intron	0.236	0.473	T	0.477
<b>rs2851392</b>	44489977	G/T	Intron	-	-	T	0.345
rs34040148	44488631	A/C	Coding exon [K102Q]	-	-	C	0.000
<b>rs3788050</b>	44474663	G/T	Intron	0.036	0.309	T	0.082
rs3788053	44484723	A/G	Intron	0.068	0.116	G	0.023
rs397589	44490214	G/T	Intron	0.114	0.119	G	0.021
<b>rs4920037</b>	44481891	A/G	Intron	0.014	0.225	A	0.175
<b>rs6586281</b>	44478393	A/G	Intron (boundary)	-	-	A	0.078
<b>rs6586282</b>	44478497	C/T	Intron	0.000	0.255	T	0.077
rs6586283	44478680	C/T	Intron	0.318	0.318	C	0.005
<b>rs706208</b>	44473446	C/T	3' UTR	0.134	0.500	C	0.385
rs7276016	44489664	A/G	Intron	-	-	A	0.035
rs760124	44475953	A/G	Intron	-	-	G	0.012
rs8131163	44488031	C/T	Intron	-	-	T	0.000
<b>rs8132811</b>	44475877	C/T	Intron	0.080	0.373	T	0.130
rs9978863	44483233	A/G	Intron (boundary)	-	-	A	0.000
rs9982015	44490092	C/T	Intron	0.000	0.164	C	0.037
rs9983620	44493201	A/G	Intron	-	-	G	0.000
<b>CYBA 16q24.3</b>							
<b>rs12709102</b>	88712319	A/G	Intron	0.084	0.464	G	0.316
rs12933505	88712767	A/G	Intron	0.092	0.494	G	0.000
rs13306295	88712618	C/T	Intron (boundary)	-	-	T	0.000
<b>rs13306296</b>	88717957	C/T	Promoter	-	-	T	0.098
rs16966653	88710636	C/G	Intron	-	-	G	0.000
rs3180279	88710833	C/G	Intron	0.167	0.454	G	0.384
rs3199601	88710095	C/T	Intron	-	-	T	0.042
<b>rs3794624</b>	88717074	A/G	Intron	0.108	0.405	A	0.107
<b>rs4782391</b>	88711466	A/G	Intron	-	-	A	0.076
rs4782393	88713501	A/G	Intron (boundary)	-	-	G	0.437
<b>rs9925947</b>	88709343	A/G	Downstream	-	-	A	0.318
rs9940427	88711819	G/T	Intron	0.000	0.032	T	0.004
<b>GSTM1 1p13.3</b>							
<b>rs1634252</b>	110228690	A/G	Promoter	-	-	A	0.396
rs2071487	110233081	C/T	Intron (boundary)	0.291	0.307	T	0.427
rs2239892	110234286	C/T	Intron	0.039	0.139	C	0.147
rs412543	110229944	C/G	Promoter	0.054	0.218	C	0.039
rs4147563	110230103	C/T	Promoter	-	-	T	0.323
rs4147567	110232524	A/G	Intron	0.000	0.134	G	0.133
rs737497	110231592	A/G	Intron (boundary)	-	-	G	0.287
<b>GSTO1 10q25.1</b>							
<b>rs1147611</b>	106025258	A/C	Intron	0.121	0.435	A	0.302
<b>rs11509438</b>	106027059	A/G	Coding exon [E208K]	0.006	0.096	A	0.101
<b>rs17116736</b>	106023387	A/G	Intron	-	-	G	0.012
rs2282326	106020398	A/C	Intron	0.187	0.435	C	0.300
<b>rs4925</b>	106022789	A/C	Coding exon [A140D]	0.042	0.383	A	0.168
<b>GSTP1 11q13.2</b>							
rs1138272	67353579	C/T	Coding exon	0.000	0.096	T	0.048
<b>rs1695</b>	67352689	A/G	Coding exon	0.098	0.494	G	0.244
<b>rs4147581</b>	67351585	C/G	Intron (boundary)	0.065	0.472	C	0.324
rs5031031	67354104	A/G	3' UTR	-	-	G	0.000
<b>rs6591256</b>	67349899	A/G	Promoter	0.098	0.465	G	0.258
<b>rs749174</b>	67353253	C/T	Intron	0.079	0.451	T	0.213
rs8191431	67350054	C/T	Promoter	0.000	0.213	T	0.000
rs8191439	67351297	A/G	5' UTR	0.004	0.362	A	0.000
rs8191446	67351827	C/G	Intron	0.000	0.213	C	0.000

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rs8191449	67352381	A/G	Intron	-	-	A	0.000
<b>rs947895</b>	67354406	A/C	Downstream	0.079	0.458	A	0.212
<b>GSTT1 22q11.23</b>							
rs2234953	24376833	A/G	Downstream	-	-	A	0.001
rs2266635	24384171	A/G	Coding exon [A21T]	0.005	0.015	A	0.012
rs4630	24376322	C/T	Downstream	-	-	C	0.067
<b>HMOX1 22q12.3</b>							
rs11555832	35789869	C/T	3' UTR	0.011	0.431	C	0.000
<b>rs11912889</b>	35783617	A/G	Intron	0.029	0.476	A	0.087
<b>rs16995662</b>	35784998	A/G	Intron	-	-	G	0.080
rs17879606	35782659	C/T	Intron (boundary)	-	-	T	0.007
rs17880294	35783286	C/T	Intron	-	-	T	0.000
rs17882597	35786008	I/D <sup>c</sup>	Intron	-	-	D	0.000
rs17885185	35783776	C/T	Intron	-	-	T	0.000
<b>rs17885522</b>	35777856	A/C	Intron	-	-	A	0.095
rs17885925	35779223	C/T	Intron (boundary)	-	-	C	0.006
rs17886055	35787065	C/T	Intron	-	-	C	0.007
rs2003038	35788909	C/T	Intron	-	-	T	0.000
<b>rs2071748</b>	35777618	A/G	Intron	0.277	0.494	G	0.464
<b>rs2071749</b>	35783413	A/G	Intron	0.009	0.469	A	0.298
<b>rs2269534</b>	35786226	C/T	Intron	-	-	C	0.433
<b>rs2285112</b>	35789263	A/G	Intron	0.223	0.494	A	0.466
<b>rs4820192</b>	35777984	A/C	Intron	-	-	C	0.441
rs5755713	35782989	C/G	Coding exon [Q152H]	-	-	C	0.000
rs5755718	35786722	C/T	Intron	-	-	C	0.173
<b>rs5755720</b>	35786873	A/G	Intron	0.130	0.493	G	0.433
<b>rs5995098</b>	35787167	C/G	Intron	0.073	0.419	G	0.432
<b>rs5995099</b>	35787235	C/T	Intron	-	-	T	0.433
<b>rs6518952</b>	35782513	C/T	Intron	0.000	0.491	T	0.080
<b>rs8139532</b>	35779568	A/G	Intron	0.024	0.407	A	0.085
rs8140370	35779635	G/T	Intron	0.000	0.241	G	0.000
<b>rs8140669</b>	35779844	A/T	Intron	0.000	0.435	A	0.080
rs9607267	35781207	C/T	Intron	0.306	0.438	C	0.471
<b>rs9622194</b>	35786963	A/G	Intron	-	-	A	0.080
<b>ICAM1 19p13.2</b>							
<b>rs281432</b>	10390658	C/G	Intron	0.250	0.482	C	0.495
rs281433	10392223	A/C	Intron	0.000	0.127	C	0.002
<b>rs3093032</b>	10396336	C/T	Promoter	0.000	0.153	T	0.093
rs5030340	10382281	C/T	Intron	0.000	0.073	T	0.050
rs5030351	10385417	C/T	Intron (boundary)	0.000	0.301	T	0.001
rs5030354	10387766	A/C	Intron	-	-	C	0.000
rs5030362	10389562	A/C	Intron	-	-	A	0.000
rs5490	10381827	A/C	5' UTR	0.000	0.250	C	0.000
rs5493	10394794	G/T	Promoter	-	-	T	0.003
rs5495	10395096	A/G	Promoter	0.000	0.006	A	0.001
rs5496	10395447	A/G	Promoter	0.000	0.489	A	0.000
<b>rs5498</b>	10395683	A/G	Promoter	0.084	0.494	G	0.429
<b>IL6 7p15.3</b>							
rs11544633	22769164	C/T	Coding exon [L119P]	-	-	C	0.000
rs13306435	22771039	A/T	Coding exon [D162E]	0.000	0.036	A	0.011
<b>rs1474347</b>	22768124	G/T	Intron	0.006	0.469	G	0.125
<b>rs1524107</b>	22768219	C/T	Intron (boundary)	0.037	0.374	T	0.421
rs1548216	22769773	C/G	Intron	0.000	0.208	C	0.050
<b>rs1554606</b>	22768707	G/T	Intron	0.006	0.464	T	0.177
rs2069830	22767137	C/T	Coding exon [P32S]	0.000	0.106	T	0.000
<b>rs2069832</b>	22767433	A/G	Intron	0.007	0.473	A	0.119
<b>rs2069835</b>	22767871	C/T	Intron	0.000	0.111	C	0.069
rs2069838	22768479	C/T	Intron (boundary)	0.000	0.097	T	0.000
<b>rs2069840</b>	22768572	C/G	Intron	0.064	0.318	G	0.142
rs2069842	22769310	A/G	Intron (boundary)	0.000	0.116	A	0.000
rs2069843	22769994	A/G	Intron	0.000	0.144	A	0.049
<b>rs2069845</b>	22770149	A/G	Intron	0.000	0.446	G	0.177
rs2069847	22770608	A/G	Intron	-	-	A	0.005

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rs2069849	22771156	C/T	Coding exon [F201F]	0.000	0.185	T	0.049
rs4335044	22765884	A/T	Promoter	0.000	0.000	T	0.000
<b>MTHFR 1p36.22</b>							
<b>rs11121832</b>	11860120	C/T	Intron	0.073	0.351	T	0.237
<b>rs12121543</b>	11854671	A/C	Intron (boundary)	0.097	0.337	A	0.361
rs13306560	11866183	A/G	Promoter	0.000	0.051	A	0.065
rs1413355	11862935	A/G	Intron (boundary)	-	-	G	0.000
<b>rs1476413</b>	11852300	A/G	Intron (boundary)	0.111	0.440	A	0.444
rs1537516	11847861	C/T	3' UTR	0.043	0.217	T	0.287
rs17037388	11858036	A/G	Intron	-	-	G	0.265
<b>rs17037390</b>	11860843	A/G	Intron	0.075	0.223	A	0.273
rs17037404	11863277	A/G	Intron (boundary)	0.000	0.097	A	0.027
rs17367504	11862778	A/G	Intron	0.075	0.175	G	0.253
rs17367629	11865236	C/T	Intron	-	-	T	0.240
<b>rs17421462</b>	11856847	A/G	Intron	0.000	0.122	A	0.077
<b>rs17421511</b>	11857788	A/G	Intron	0.009	0.234	A	0.156
<b>rs1801131</b>	11854476	A/C	Coding exon [E429A]	0.111	0.392	C	0.415
<b>rs1801133</b>	11856378	C/T	Coding exon [A222V]	0.080	0.475	T	0.109
<b>rs1994798</b>	11854755	C/T	Intron (boundary)	0.189	0.479	C	0.493
rs2066461	11861348	A/C	Coding exon [T115T]	0.006	0.006	A	0.000
rs2066466	11861276	A/G	Coding exon [T139T]	0.005	0.021	A	0.000
<b>rs2066471</b>	11860458	A/G	Intron (boundary)	0.000	0.179	A	0.157
rs2077360	11848879	A/G	3' UTR	-	-	A	0.000
<b>rs2184226</b>	11847436	A/G	3' UTR	0.000	0.140	G	0.068
rs28484963	11847742	G/T	3' UTR	-	-	G	0.000
<b>rs3737965</b>	11866451	C/T	Promoter	0.055	0.093	T	0.165
<b>rs3753582</b>	11865542	G/T	Intron	0.065	0.134	G	0.191
<b>rs3753584</b>	11864586	A/G	Intron	0.075	0.176	G	0.260
rs3753588	11863904	A/G	Intron	-	-	A	0.228
rs41452445	11858584	A/G	Intron	-	-	G	0.023
rs4845884	11846447	A/G	3' UTR	0.000	0.264	G	0.000
rs4846048	11846252	A/G	3' UTR	0.073	0.482	G	0.032
<b>rs4846049</b>	11850365	G/T	3' UTR	0.186	0.482	T	0.474
rs4846050	11852969	C/T	Intron	-	-	T	0.001
<b>rs4846052</b>	11857951	C/T	Intron	0.148	0.500	T	0.490
<b>rs6541003</b>	11855867	A/G	Intron	0.177	0.500	G	0.499
rs6700268	11851950	C/G	Intron	0.000	0.051	C	0.000
rs7518348	11851118	A/G	Intron	0.000	0.380	A	0.005
<b>rs7533315</b>	11860683	C/T	Intron	0.081	0.313	T	0.239
rs7547068	11862331	A/G	Intron	-	-	A	0.000
<b>rs9651118</b>	11862214	C/T	Intron	0.000	0.414	C	0.329
<b>NOS3 7q36.1</b>							
rs1008140	150705610	C/T	Intron	-	-	C	0.043
rs1541861	150697333	A/C	Intron	-	-	C	0.261
<b>rs1800779</b>	150689943	A/G	Promoter	0.073	0.468	G	0.219
<b>rs1800783</b>	150689397	A/T	Promoter	0.058	0.418	A	0.224
<b>rs1808593</b>	150708302	G/T	Downstream	0.135	0.240	G	0.183
<b>rs2853792</b>	150699877	A/G	Intron	-	-	G	0.310
rs2853795	150703242	A/G	Intron	-	-	G	0.226
<b>rs3793342</b>	150695195	C/T	Intron	0.066	0.205	T	0.159
<b>rs3834873</b>	150703742/43	I/D <sup>c</sup>	Intron	-	-	I	0.166
rs3918166	150693556	A/G	Coding exon [R112Q]	0.000	0.121	G	0.000
<b>rs3918169</b>	150694606	A/G	Intron	-	-	G	0.200
rs3918171	150697095	A/G	Intron	-	-	A	0.047
<b>rs3918181</b>	150701783	A/G	Intron	-	-	A	0.304
<b>rs3918186</b>	150702432	A/T	Intron	0.069	0.167	T	0.161
<b>rs3918188</b>	150702781	A/C	Intron	0.178	0.425	A	0.323
rs3918194	150705200	I/D <sup>c</sup>	Intron	-	-	D	0.000
rs3918198	150706377	A/C	Intron (boundary)	-	-	A	0.000
<b>rs3918204</b>	150708459/60	I/D <sup>c</sup>	Intron	-	-	D	0.185
rs3918226	150690176	C/T	Promoter	-	-	T	0.004
<b>rs3918227</b>	150700946	A/C	Intron	0.000	0.135	A	0.066
<b>rs6951150</b>	150681914	C/T	Promoter	0.000	0.455	T	0.222

db SNP ID <sup>a</sup>	SNP position	Alleles	Role [amino acid change]	Prior studies min MAF <sup>b</sup>	Prior studies max MAF <sup>b</sup>	Present study minor allele	Present study MAF
<b>rs743506</b>	150706915	A/G	Intron	0.149	0.476	G	0.190
<b>rs743507</b>	150707488	A/G	Intron	0.139	0.403	G	0.189
rs7830	150709571	A/C	3' UTR	0.122	0.445	A	0.436
<b>rs891512</b>	150708089	A/G	Downstream	0.000	0.296	A	0.140
<b>PNP 14q11.2</b>							
<b>rs1049562</b>	20940515	A/G	Coding exon [H20H]	0.106	0.265	A	0.137
<b>rs1049564</b>	20940606	C/T	Coding exon [G51S]	0.121	0.350	T	0.139
rs12101049	20939701	A/G	Intron	-	-	A	0.000
<b>rs1617940</b>	20941413	A/T	Intron	0.241	0.346	T	0.161
rs17112168	20936978	A/C	Promoter	-	-	A	0.008
<b>rs1713420</b>	20942744	C/T	Intron (boundary)	0.093	0.362	C	0.139
<b>rs1713421</b>	20942451	A/C	Intron	0.094	0.362	C	0.142
<b>rs1756369</b>	20943504	A/T	Intron (boundary)	0.139	0.381	T	0.159
rs1760933	20945488	A/G	3' UTR	-	-	A	0.044
<b>rs1760935</b>	20941613	C/T	Intron	0.122	0.457	C	0.137
<b>rs1760940</b>	20938251	G/T	Intron	0.102	0.233	G	0.141
rs17878900	20945355	C/T	3' UTR	-	-	T	0.035
rs17879107	20940360	G/T	Intron	-	-	G	0.018
rs17880290	20937412	A/G	Promoter	-	-	A	0.029
rs17880503	20935743	C/T	Promoter	-	-	C	0.013
rs17881184	20943565	A/G	Intron	-	-	G	0.000
rs17881554	20943281	A/T	Coding exon [A174A]	-	-	A	0.000
<b>rs17882804</b>	20941303/04	I/D <sup>c</sup>	Intron	-	-	I	0.158
rs17882836	20939039	A/G	Intron	-	-	A	0.008
rs17883795	20945571	A/G	3' UTR	-	-	A	0.020
rs17885714	20941715	A/G	Intron	-	-	G	0.023
rs17885781	20938710/11	I/D <sup>c</sup>	Intron	-	-	D	0.000
rs17885917	20940735	A/G	Intron (boundary)	-	-	G	0.012
rs17886095	20940798	A/G	Intron	-	-	A	0.019
rs3790062	20937111	A/G	Promoter	0.000	0.037	A	0.008
rs3790064	20941069	A/G	Intron	0.014	0.134	G	0.038
<b>S1PR1 1p21.2</b>							
<b>rs1411017</b>	101703249	A/G	Intron	0.045	0.417	G	0.090
<b>rs17100954</b>	101704029	A/G	Intron	0.065	0.067	A	0.091
<b>rs3737577</b>	101704532	A/C	5' UTR	0.018	0.306	A	0.096
<b>rs3753194</b>	101702825	C/T	Intron	0.012	0.371	C	0.071
rs4987248	101702546	C/G	5' UTR	0.046	0.244	C	0.077
rs7549921	101705535	C/G	Coding exon [P332R]	0.000	0.000	G	0.000
<b>SOD2 6q25.3</b>							
rs10370	160101532	A/C	Intron	-	-	C	0.321
rs12195992	160109524	C/G	Intron	-	-	G	0.000
rs12526686	160112013	C/T	Intron	-	-	T	0.000
rs1800665	160107091	A/G	Intron	-	-	A	0.002
<b>rs1800666</b>	160110140	A/G	Intron	-	-	A	0.264
<b>rs2758331</b>	160105070	A/C	Intron	0.116	0.461	C	0.482
<b>rs2758332</b>	160106088	A/C	Intron (boundary)	-	-	C	0.469
<b>rs2758334</b>	160110454	C/T	Intron	-	-	T	0.482
rs2758340	160112709	A/C	Intron	-	-	A	0.000
rs2758345	160114793	C/G	Promoter	-	-	G	0.001
<b>rs2842960</b>	160113321	C/T	Intron	0.116	0.474	C	0.465
rs3798215	160104838	A/G	Intron	-	-	G	0.241
<b>rs5746088</b>	160114726	A/G	Promoter	-	-	A	0.052
rs5746099	160113599	A/C	Intron (boundary)	-	-	C	0.000
rs5746104	160112855	C/G	Intron	-	-	G	0.048
<b>rs5746105</b>	160112638	C/T	Intron	0.181	0.420	C	0.321
rs5746108	160112560	A/G	Intron	-	-	A	0.000
rs5746109	160112496	A/G	Intron	-	-	G	0.007
rs5746110	160112387	A/G	Intron	-	-	G	0.000
rs5746111	160109611	C/G	Intron	-	-	C	0.005
rs5746114	160108721	A/G	Intron	-	-	G	0.000
rs5746123	160106703	A/G	Intron	-	-	A	0.000
<b>rs5746136</b>	160103084	A/G	Intron	0.152	0.421	A	0.306
rs5746141	160102710	A/G	Intron	0.000	0.086	A	0.038

db SNP ID <sup>a</sup>	SNP position	Alleles	Role [amino acid change]	Prior studies min MAF <sup>b</sup>	Prior studies max MAF <sup>b</sup>	Present study minor allele	Present study MAF
<b>rs6912979</b>	160120799	C/T	Promoter	0.200	0.421	C	0.291
<b>rs8031</b>	160100640	A/T	Intron	0.116	0.461	T	0.485
rs9457709	160111917	A/G	Intron	-	-	A	0.000
<b>TNF 6p21.33</b>							
rs17207127	31541948	C/T	3' UTR	-	-	T	0.007
rs17207134	31542113	C/T	Downstream	-	-	C	0.000
<b>rs1799964</b>	31542308	C/T	Downstream	-	-	C	0.358
rs1800610	31543827	C/T	Intron	-	-	T	0.074
<b>rs1800630</b>	31542476	A/C	Downstream	-	-	A	0.268
rs2228088	31543605	G/T	Coding exon [R29R]	0.000	0.065	T	0.000
rs3093544	31541779	A/G	3' UTR	-	-	G	0.000
rs3093547	31541848	A/T	3' UTR	-	-	A	0.044
<b>rs3093661</b>	31543758	A/G	Intron	0.003	0.163	A	0.093
<b>rs3093662</b>	31544189	A/G	Intron	0.018	0.189	G	0.104
<b>rs3093664</b>	31544642	A/G	Intron	-	-	G	0.106
rs3093665	31545391	A/C	3' UTR	0.004	0.061	C	0.010
rs3179060	31543672	A/C	Coding exon [H52N]	-	-	A	0.000
rs4248159	31542580	A/C	Downstream	-	-	A	0.001
rs4645843	31544562	C/T	Coding exon [P84L]	0.000	0.010	T	0.000
<b>VCAM1 1p21.2</b>							
rs1041163	101183825	C/T	Promoter	0.071	0.186	C	0.177
<b>rs1409419</b>	101183396	C/T	Promoter	0.355	0.411	T	0.401
<b>rs2209627</b>	101199147	A/G	Intron	0.011	0.116	G	0.072
<b>rs2392221</b>	101190173	C/T	Intron (boundary)	-	-	T	0.173
rs3170794	101184584	C/T	Promoter	0.000	0.153	C	0.003
rs3176859	101186870	G/T	Intron	-	-	T	0.035
<b>rs3176860</b>	101187219	A/G	Intron	0.305	0.500	A	0.433
<b>rs3176861</b>	101187321	C/T	Intron	0.010	0.256	T	0.399
rs3176862	101187972	C/G	Intron	0.000	0.164	G	0.003
rs3176863	101188192	A/G	Intron	0.037	0.337	A	0.182
<b>rs3176867</b>	101194205	C/T	Intron	0.005	0.372	T	0.287
<b>rs3176870</b>	101197183	A/G	Intron	0.009	0.250	A	0.087
<b>rs3176871</b>	101197289	A/G	Intron	0.012	0.093	A	0.051
<b>rs3176874</b>	101199886	A/G	Intron	0.036	0.281	G	0.184
rs3176876	101200608	A/G	Intron	0.250	0.436	G	0.384
<b>rs3176877</b>	101203395	A/T	Intron	0.278	0.500	A	0.450
<b>rs3176878</b>	101203698	C/T	Coding exon [D601D]	0.000	0.234	T	0.071
rs3181087	101184175	A/T	Promoter	0.000	0.053	T	0.000
<b>rs3181088</b>	101198708	C/T	Intron	0.000	0.191	T	0.138
rs3181089	101198826	C/T	Intron	0.000	0.115	T	0.000
<b>rs3181092</b>	101204644	A/G	Downstream	0.241	0.500	A	0.435
<b>rs3765685</b>	101192993	A/G	Intron	0.071	0.149	G	0.168
rs3783597	101183724	C/G	Promoter	0.000	0.019	G	0.000
rs3783599	101183887	C/T	Promoter	0.000	0.073	T	0.000
rs3783601	101184061	A/G	Promoter	0.000	0.027	G	0.000
rs3783603	101184269	A/G	Promoter	0.000	0.019	A	0.000
rs3783606	101185034	G/T	Promoter	0.000	0.000	G	0.000
rs3783609	101185363	A/G	5' UTR	0.000	0.116	A	0.000
rs3783613	101196787	C/G	Coding exon [G321A]	0.000	0.173	C	0.000
rs3783617	101203881	C/G	3' UTR	-	-	C	0.000
rs3783624	101204798	A/G	Downstream	0.000	0.036	G	0.000
rs3917009	101189410	C/T	Intron	0.030	0.125	T	0.022
<b>rs3917010</b>	101190866	A/C	Intron	0.000	0.250	C	0.425
rs3917014	101197384	A/G	Intron	0.009	0.244	A	0.452
<b>rs3917016</b>	101201147	A/T	Intron	0.036	0.227	A	0.180
<b>rs3917018</b>	101202222	A/G	Intron	0.245	0.500	A	0.443
<b>rs3917019</b>	101202354	A/G	Intron	0.259	0.417	A	0.289
<b>rs3917022</b>	101204883	C/T	Downstream	0.027	0.148	C	0.175
rs3917026	101184824	C/T	Promoter	0.000	0.033	C	0.000
rs3917032	101187123	A/C	Intron	-	-	A	0.000
rs3917033	101187613	C/T	Intron	-	-	C	0.000
rs3917057	101196175	A/G	Intron	0.000	0.048	G	0.000

<sup>a</sup>SNPs that were included in the final analysis ( $n = 170$ ) are bolded. The remaining SNPs were excluded because of poor genotyping efficiency (< 95%), monomorphic genotype data, deviation from Hardy-Weinberg equilibrium (< 0.0001), or low MAF (< 5%). <sup>b</sup><http://snpper.chip.org/bio/snpper-enter/>. SNPper is a web-based tool to retrieve known SNPs from public databases. MAF data are not available in SNPper for some of the known SNPs. <sup>c</sup>Insertion/deletion polymorphism.

**Table S2.** Characteristics of the subcohort in the present study ( $n = 1,375$ ) and participants in the overall cohort study ( $n = 20,033$ ) [ $n$  (%)] or mean  $\pm$  SD].

Characteristic	Subcohort <sup>a</sup>	Overall cohort participants
Sex		
Women	800 (58.2)	11870 (59.3)
Men	575 (41.8)	8163 (40.8)
Age (years)	38.6 $\pm$ 9.7	36.9 $\pm$ 10.4
Body mass index (kg/m <sup>2</sup> )	19.9 $\pm$ 3.3	19.8 $\pm$ 3.2
Education (years)	3.1 $\pm$ 3.7	3.5 $\pm$ 3.8
Smoking status		
Never	877 (63.8)	13510 (67.5)
Past	90 (6.6)	1255 (6.3)
Current	408 (29.7)	5260 (26.3)
Systolic blood pressure (mmHg)	116.5 $\pm$ 17.3	116.6 $\pm$ 17.2
Diastolic blood pressure (mmHg)	75.0 $\pm$ 10.9	74.9 $\pm$ 11.2
Well arsenic (µg/L)	80.8 $\pm$ 101.3	81.7 $\pm$ 105.9
Urinary arsenic (µg/L)	114.9 $\pm$ 131.8	118.7 $\pm$ 144.5
Urinary creatinine (mg/dL)	54.0 $\pm$ 42.7	53.8 $\pm$ 42.6
Urinary arsenic (µg/g creatinine)	257.6 $\pm$ 322.0	259.2 $\pm$ 285.3

<sup>a</sup>The subcohort included 56 CVD cases.

**Table S3.** Association between baseline well-water arsenic and CVD, CHD, and stroke.

Well-water arsenic ( $\mu\text{g/L}$ )	Mean <sup>a</sup>	Subcohort <sup>b</sup> (n)	CVD cases (n)	CVD aHR (95% CI) <sup>c</sup>	CHD cases (n)	CHD aHR (95% CI) <sup>c</sup>	Stroke cases (n)	Stroke aHR (95% CI) <sup>c</sup>
0.1-16	4.3	453	125	1.00	69	1.00	44	1.00
17-85	46.7	452	147	1.24 (0.84, 1.84)	86	1.30 (0.83, 2.01)	50	1.14 (0.65, 1.98)
86-864	191.2	454	174	1.69 (1.15, 2.50)	82	1.40 (0.88, 2.23)	71	1.87 (1.06, 3.29)
Per SD (101.3 $\mu\text{g/L}$ )		1359	446	1.21 (1.08, 1.37)	237	1.17 (1.01, 1.35)	165	1.19 (1.02, 1.40)

<sup>a</sup>Category-specific mean values of well-water arsenic in the subcohort. <sup>b</sup>Data on well-water arsenic were missing on 16 subjects in the subcohort.

<sup>c</sup>Adjusted for sex, age, BMI, smoking status (never, past, and current), educational attainment, systolic blood pressure, diabetes status, and change in creatinine-adjusted urinary arsenic between visits.

**Table S4.** Nominally significant interactions between well-water arsenic and SNPs in CHD and stroke.

db SNP ID	Genotype	MAF (%)	aHR (95%CI) well-water arsenic <sup>a</sup>	aHR (95%CI) SNP <sup>a</sup>	aHR (95%CI) joint <sup>a</sup>	P <sup>b</sup>	P <sub>adj</sub> <sup>c</sup>
<b>CHD</b>							
<i>AS3MT</i>							
rs1046778	TC+CC vs. TT	C (34.8)	0.96 (0.74, 1.24)	0.96 (0.63, 1.46)	1.25 (0.84, 1.85)	0.043	0.315
rs11191454	AG+GG vs. AA	G (17.2)	1.06 (0.88, 1.26)	0.91 (0.55, 1.52)	1.33 (0.88, 2.01)	0.036	0.290
rs12573221	AC+CC vs. AA	C (12.1)	1.05 (0.87, 1.27)	0.72 (0.43, 1.22)	1.17 (0.76, 1.78)	0.007	0.257
<i>CBS</i>							
rs1005585	AG+GG vs. AA	G (7.8)	1.10 (0.93, 1.29)	0.48 (0.24, 0.96)	0.93 (0.55, 1.58)	0.009	0.257
rs11700748	TC+TT vs. CC	T (38.9)	0.86 (0.62, 1.19)	0.79 (0.50, 1.23)	1.04 (0.68, 1.58)	0.018	0.257
rs2124459	TC+CC vs. TT	C (41.1)	0.91 (0.65, 1.27)	0.83 (0.50, 1.35)	1.08 (0.67, 1.73)	0.050	0.321
rs2849727	TC+TT vs. CC	T (33.9)	0.92 (0.69, 1.24)	0.84 (0.55, 1.29)	1.08 (0.72, 1.61)	0.050	0.321
rs3788050	GT+TT vs. GG	T (8.2)	1.09 (0.93, 1.29)	0.52 (0.27, 1.01)	0.96 (0.58, 1.58)	0.018	0.257
rs706208	TC+CC vs. TT	C (38.5)	0.88 (0.63, 1.24)	0.77 (0.49, 1.21)	1.02 (0.67, 1.56)	0.031	0.275
<i>GSTO1</i>							
rs1147611	CA+AA vs. CC	A (30.2)	0.98 (0.77, 1.25)	1.25 (0.80, 1.95)	1.72 (1.13, 2.60)	0.028	0.275
rs11509438	GA+AA vs. GG	A (10.1)	1.11 (0.94, 1.32)	1.23 (0.72, 2.09)	2.07 (1.36, 3.15)	0.028	0.275
rs2282326	AC+CC vs. AA	C (30.0)	1.00 (0.80, 1.26)	1.27 (0.82, 1.97)	1.74 (1.15, 2.63)	0.036	0.290
<i>ICAM1</i>							
rs281432	GG vs. CG+CC	C (49.5)	1.06 (0.89, 1.27)	0.95 (0.59, 1.55)	1.56 (1.04, 2.34)	0.007	0.257
<i>IL6</i>							
rs2069835	TC+CC vs. TT	C (6.9)	1.10 (0.94, 1.30)	0.74 (0.40, 1.39)	1.27 (0.77, 2.12)	0.031	0.275
<i>MTHFR</i>							
rs12121543	CA+AA vs. CC	A (36.1)	0.92 (0.68, 1.24)	0.65 (0.41, 1.02)	0.92 (0.61, 1.39)	0.016	0.257
rs17421462	GG vs. GA+AA	A (7.7)	0.75 (0.49, 1.15)	0.64 (0.37, 1.11)	0.80 (0.47, 1.36)	0.029	0.275
rs1801131	AC+CC vs. AA	C (41.5)	0.84 (0.58, 1.22)	0.66 (0.41, 1.06)	0.92 (0.59, 1.43)	0.015	0.257
<i>NOS3</i>							
rs1800783	TA+AA vs. TT	A (22.4)	0.98 (0.77, 1.23)	0.67 (0.43, 1.05)	0.94 (0.63, 1.39)	0.015	0.257
rs6951150	TC+TT vs. CC	T (22.2)	0.97 (0.77, 1.24)	0.68 (0.44, 1.07)	0.96 (0.65, 1.44)	0.014	0.257
<i>SOD2</i>							
rs2758334	TC+CC vs. TT	T (48.2)	0.87 (0.61, 1.26)	0.72 (0.45, 1.17)	0.96 (0.61, 1.51)	0.042	0.315
<i>VCAM1</i>							
rs1409419	CC vs. TC+TT	T (40.1)	1.07 (0.86, 1.32)	0.54 (0.33, 0.88)	0.83 (0.56, 1.24)	0.027	0.275
rs2209627	AA vs. AG+GG	G (7.2)	0.61 (0.37, 1.01)	0.57 (0.32, 1.00)	0.70 (0.40, 1.23)	0.008	0.257

db SNP ID	Genotype	MAF (%)	aHR (95%CI) well-water arsenic <sup>a</sup>	aHR (95%CI) SNP <sup>a</sup>	aHR (95%CI) joint <sup>a</sup>	P <sup>b</sup>	P <sub>adj</sub> <sup>c</sup>
rs3176867	CC vs. TC+TT	T (28.7)	1.03 (0.82, 1.29)	1.05 (0.68, 1.62)	1.51 (1.01, 2.26)	0.027	0.275
rs3176871	GG vs. GA+AA	A (5.1)	0.76 (0.53, 1.08)	0.39 (0.21, 0.71)	0.48 (0.27, 0.88)	0.011	0.257
rs3176878	CC vs. TC+TT	T (7.1)	0.65 (0.40, 1.07)	0.63 (0.36, 1.11)	0.78 (0.45, 1.35)	0.014	0.257
rs3917014	GG vs. AG+AA	A (45.2)	1.12 (0.96, 1.31)	0.75 (0.36, 1.56)	1.55 (0.87, 2.73)	0.003	0.260
<b>Stroke</b>							
<i>AS3MT</i>							
rs10786719	AG+GG vs. AA	G (43.8)	0.82 (0.52, 1.28)	0.88 (0.48, 1.61)	1.16 (0.64, 2.08)	0.050	0.440
rs11191439	TT vs. TC+CC	C (5.4)	0.70 (0.41, 1.20)	0.66 (0.30, 1.44)	0.82 (0.38, 1.76)	0.044	0.440
<i>CBS</i>							
rs8132811	CT+TT vs. CC	T (13.0)	1.14 (0.95, 1.36)	0.55 (0.29, 1.04)	0.97 (0.57, 1.64)	0.021	0.440
<i>GSTO1</i>							
rs1147611	CA+AA vs. CC	A (30.2)	1.00 (0.77, 1.29)	1.15 (0.67, 1.98)	1.64 (0.99, 2.73)	0.027	0.440
<i>ICAM1</i>							
rs281432	GG vs. CG+CC	C (49.5)	1.08 (0.90, 1.31)	0.92 (0.52, 1.61)	1.85 (1.14, 3.01)	8.3×10 <sup>-5</sup>	0.014
<i>NOS3</i>							
rs1800779	AG+GG vs. AA	G (21.9)	1.03 (0.82, 1.28)	0.96 (0.57, 1.61)	1.36 (0.84, 2.20)	0.034	0.440
rs1800783	TA+AA vs. TT	A (22.4)	0.99 (0.79, 1.24)	0.76 (0.45, 1.27)	1.10 (0.69, 1.76)	0.013	0.440
rs3793342	CT+TT vs. CC	T (15.9)	1.02 (0.82, 1.26)	0.89 (0.52, 1.55)	1.29 (0.79, 2.12)	0.023	0.440
rs3918169	AG+GG vs. AA	G (20.0)	1.03 (0.83, 1.28)	0.82 (0.48, 1.40)	1.18 (0.73, 1.92)	0.031	0.440
rs6951150	CT+TT vs. CC	T (22.2)	0.93 (0.74, 1.17)	0.67 (0.40, 1.14)	1.01 (0.63, 1.62)	0.002	0.193
<i>VCAM1</i>							
rs3176867	CC vs. TC+TT	T (28.7)	1.00 (0.78, 1.28)	0.78 (0.47, 1.30)	1.23 (0.76, 1.99)	0.007	0.377

<sup>a</sup>Adjusted HR in association with a 1-SD increase in well-water arsenic (101.3 µg/L) and “at-risk” genotype (s) of SNPs, and joint effect between well-water arsenic and SNPs, adjusting for sex, age, BMI, smoking status (never, past, and current), educational attainment, systolic blood pressure, diabetes status, and change in creatinine-adjusted urinary arsenic between visits. <sup>b</sup>Nominal P values from *1df* tests for multiplicative interactions between a 1-SD increase well-water arsenic and SNPs. <sup>c</sup>FDR adjusted P values.

**Table S5.** Nominally significant interactions between urinary creatinine-adjusted arsenic and SNPs in CVD, CHD, and stroke.

<b>db SNP ID</b>	<b>Genotype</b>	<b>MAF (%)</b>	<b>aHR (95%CI) urinary arsenic<sup>a</sup></b>	<b>aHR (95%CI) SNP<sup>a</sup></b>	<b>aHR (95%CI) joint<sup>a</sup></b>	<b>P<sup>b</sup></b>
<b>CVD</b>						
<i>AS3MT</i>						
rs12573221	AC+CC vs. AA	C (12.1)	0.95 (0.71, 1.27)	0.64 (0.39, 1.05)	0.99 (0.64, 1.54)	0.011
rs4290163	GT+TT vs. GG	T (42.2)	0.81 (0.56, 1.18)	0.78 (0.50, 1.23)	1.11 (0.72, 1.70)	0.011
<i>CBS</i>						
rs1005585	AG+GG vs. AA	G (7.8)	1.01 (0.75, 1.35)	0.44 (0.25, 0.76)	1.02 (0.63, 1.64)	4.3×10 <sup>-7</sup>
rs3788050	GT+TT vs. GG	T (8.2)	1.00 (0.75, 1.33)	0.49 (0.29, 0.82)	1.09 (0.69, 1.73)	1.1×10 <sup>-6</sup>
rs8132811	CT+TT vs. CC	T (13.0)	1.00 (0.74, 1.34)	0.55 (0.35, 0.89)	1.00 (0.65, 1.54)	0.002
<i>ICAM1</i>						
rs281432	GG vs. CG+CC	C (49.5)	1.01 (0.75, 1.35)	1.16 (0.79, 1.72)	1.68 (1.12, 2.52)	0.014
<i>SOD2</i>						
rs2758331	CA+AA vs. CC	C (48.2)	0.77 (0.51, 1.15)	0.69 (0.44, 1.08)	0.97 (0.63, 1.50)	0.010
rs2758334	TC+CC vs. TT	T (48.2)	0.72 (0.49, 1.07)	0.61 (0.39, 0.95)	0.86 (0.56, 1.31)	0.005
rs8031	TA+AA vs. TT	T (48.5)	0.73 (0.49, 1.10)	0.66 (0.42, 1.02)	0.90 (0.59, 1.38)	0.008
<b>CHD</b>						
<i>AS3MT</i>						
rs12573221	AC+CC vs. AA	C (12.1)	0.95 (0.69, 1.30)	0.70 (0.41, 1.18)	1.03 (0.63, 1.69)	0.035
<i>CBS</i>						
rs1005585	AG+GG vs. AA	G (7.8)	1.01 (0.74, 1.37)	0.42 (0.21, 0.83)	1.01 (0.57, 1.79)	0.0003
rs3788050	GT+TT vs. GG	T (8.2)	0.99 (0.73, 1.35)	0.45 (0.23, 0.87)	1.02 (0.59, 1.79)	0.0009
<i>VCAM1</i>						
rs1409419	CC vs. TC+TT	T (40.1)	0.96 (0.69, 1.34)	0.47 (0.28, 0.78)	0.84 (0.54, 1.31)	0.002
rs2209627	AA vs. AG+GG	G (7.2)	0.45 (0.19, 1.08)	0.49 (0.25, 0.99)	0.57 (0.29, 1.14)	0.043
rs3176878	CC vs. TC+TT	T (7.1)	0.45 (0.18, 1.16)	0.52 (0.25, 1.05)	0.62 (0.31, 1.25)	0.050
<b>Stroke</b>						
<i>CBS</i>						
rs8132811	CT+TT vs. CC	T (13.0)	0.92 (0.63, 1.33)	0.44 (0.22, 0.90)	0.89 (0.49, 1.63)	0.003
<i>ICAM1</i>						
rs281432	GG vs. CG+CC	C (49.5)	0.96 (0.67, 1.39)	0.97 (0.55, 1.72)	1.60 (0.87, 2.93)	0.005

<sup>a</sup>Adjusted HR in association with a 1-SD increase in urinary arsenic (322 µg/g creatinine) and “at-risk” genotype (s) of SNPs, and joint effect between well-water arsenic and SNPs, adjusting for sex, age, BMI, smoking status (never, past, and current), educational attainment, systolic blood pressure, diabetes status, and change in creatinine-adjusted urinary arsenic between visits. <sup>b</sup>Nominal P values from 1df tests for multiplicative interactions between a 1-SD increase urinary arsenic and SNPs.

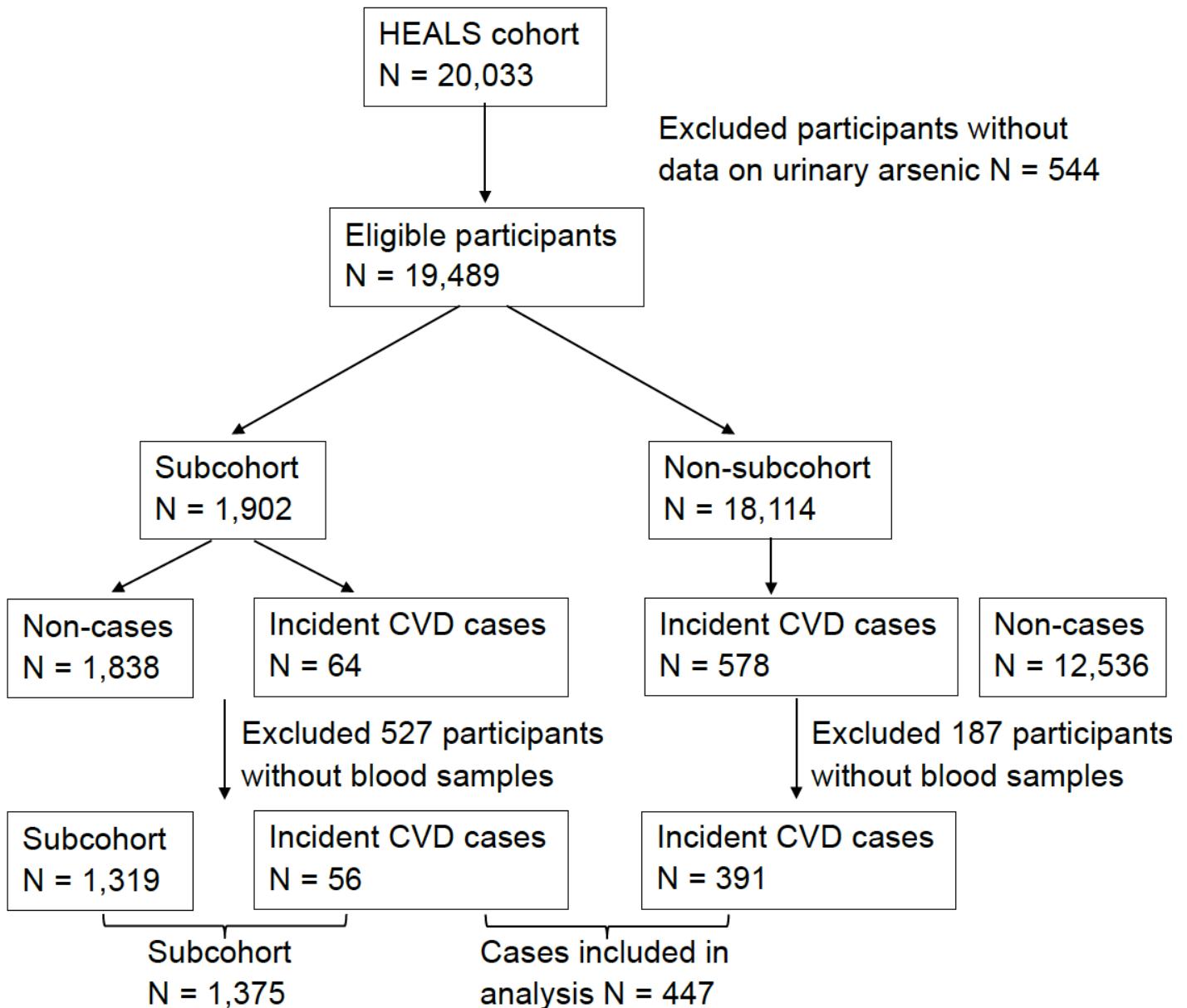
**Table S6.** Nominally significant associations between SNPs and CVD, CHD, and stroke.

<b>db SNP ID</b>	<b>Genotype</b>	<b>MAF (%)</b>	<b>aHR (95% CI)<sup>a</sup></b>	<b>P<sup>b</sup></b>	<b>P<sub>adj</sub><sup>c</sup></b>
<b>CVD</b>					
<b>AS3MT</b>					
rs10748835	AG+GG vs. AA	A (43.9)	1.44 (1.04, 1.99)	0.027	0.417
rs3740393	CG+CC vs. GG	C (18.9)	1.47 (1.09, 1.97)	0.011	0.315
<b>CBS</b>					
rs1789953	CT+TT vs. CC	T (23.8)	0.69 (0.51, 0.94)	0.018	0.384
rs234706	GA+AA vs. GG	A (20.9)	1.34 (1.01, 1.79)	0.043	0.421
<b>CYBA</b>					
rs3794624	GA+AA vs. GG	A (10.7)	1.43 (1.05, 1.95)	0.023	0.403
<b>HMOX1</b>					
rs2285112	GA+AA vs. GG	A (46.6)	0.73 (0.54, 0.99)	0.042	0.421
<b>ICAM1</b>					
rs281432	GC+CC vs. GG	C (49.5)	0.65 (0.48, 0.87)	0.004	0.176
<b>IL6</b>					
rs2069832	GA+AA vs. GG	A (11.9)	0.60 (0.40, 0.90)	0.013	0.319
<b>MTHFR</b>					
rs1801133	CT+TT vs. CC	T (10.9)	1.58 (1.16, 2.17)	0.004	0.176
<b>NOS3</b>					
rs2853792	AG+GG vs. AA	G (31.0)	0.51 (0.38, 0.69)	1.0×10 <sup>-5</sup>	0.002
<b>SOD2</b>					
rs5746088	GA+AA vs. GG	A (5.2)	0.30 (0.17, 0.51)	1.0×10 <sup>-5</sup>	0.001
rs5746136	GA+AA vs. GG	A (30.6)	1.35 (1.01, 1.79)	0.044	0.421
<b>VCAM1</b>					
rs2392221	CT+TT vs. CC	T (17.3)	0.63 (0.45, 0.89)	0.008	0.281
rs3176860	GA+AA vs. GG	A (43.3)	1.39 (1.01, 1.92)	0.044	0.421
rs3176870	GA+AA vs. GG	A (8.7)	1.49 (1.05, 2.11)	0.024	0.403
rs3176871	GA+AA vs. GG	A (5.1)	1.57 (1.01, 2.44)	0.044	0.421
<b>CHD</b>					
<b>AS3MT</b>					
rs3740393	CG+CC vs. GG	C (18.9)	1.46 (1.03, 2.08)	0.035	0.542
<b>CBS</b>					
rs1789953	CT+TT vs. CC	T (23.8)	0.65 (0.45, 0.94)	0.021	0.457
rs234705	CT+TT vs. CC	T (21.9)	1.49 (1.07, 2.10)	0.020	0.457
rs234706	GA+AA vs. GG	A (20.9)	1.50 (1.07, 2.11)	0.020	0.457
<b>CYBA</b>					
rs3794624	GA+AA vs. GG	A (10.7)	1.63 (1.11, 2.40)	0.014	0.457
<b>GSTO1</b>					
rs1147611	CA+AA vs. CC	A (30.2)	1.47 (1.05, 2.07)	0.027	0.457
rs11509438	GA+AA vs. GG	A (10.1)	1.54 (1.05, 2.26)	0.027	0.457
rs2282326	AC+CC vs. AA	C (30.0)	1.48 (1.05, 2.09)	0.025	0.457
<b>NOS3</b>					
rs2853792	AG+GG vs. AA	G (31.0)	0.49 (0.34, 0.70)	0.0001	<b>0.018</b>
<b>SOD2</b>					
rs5746088	GA+AA vs. GG	A (5.2)	0.29 (0.15, 0.58)	0.0004	<b>0.037</b>
<b>VCAM1</b>					
rs2392221	CT+TT vs. CC	T (17.3)	0.57 (0.38, 0.85)	0.006	0.312

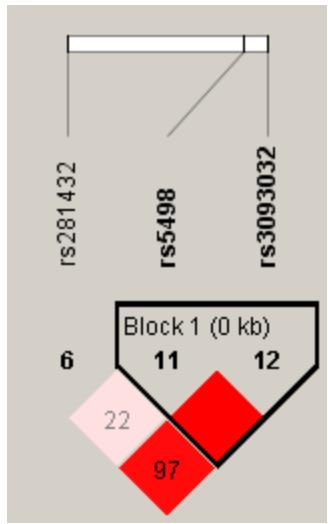
<b>db SNP ID</b>	<b>Genotype</b>	<b>MAF (%)</b>	<b>aHR (95% CI)<sup>a</sup></b>	<b>P<sup>b</sup></b>	<b>P<sub>adj</sub><sup>c</sup></b>
<b>Stroke</b>					
<i>AS3MT</i>					
rs3740393	CG+CC vs. GG	C (18.9)	1.55 (1.01, 2.37)	0.044	0.690
<i>IL6</i>					
rs2069832	GA+AA vs. GG	A (11.9)	0.53 (0.31, 0.92)	0.025	0.690
<i>MTHFR</i>					
rs17037390	GA+AA vs. GG	A (27.3)	0.63 (0.40, 0.98)	0.039	0.690
rs1801133	CT+TT vs. CC	T (10.9)	2.33 (1.51, 3.61)	0.0001	<b>0.024</b>
rs3737965	CT+TT vs. CC	T (16.5)	0.47 (0.28, 0.80)	0.006	0.475
rs3753584	AG+GG vs. AA	G (26.0)	0.61 (0.40, 0.96)	0.031	0.690
<i>NOS3</i>					
rs2853792	AG+GG vs. AA	G (31.0)	0.63 (0.41, 0.97)	0.036	0.690
<i>SOD2</i>					
rs5746088	GA+AA vs. GG	A (5.2)	0.38 (0.17, 0.84)	0.017	0.690
<i>VCAM1</i>					
rs3176870	GA+AA vs. GG	A (8.7)	1.81 (1.10, 2.99)	0.020	0.690
rs3917022	TC+CC vs. TT	C (17.5)	1.54 (1.00, 2.35)	0.049	0.690

<sup>a</sup>Adjusted HR in association with “at-risk” genotype (s) of SNPs, adjusting for sex, age, BMI, smoking status (never, past, and current), educational attainment, systolic blood pressure, and diabetes status. <sup>b</sup>Nominal P values from *1df* tests.

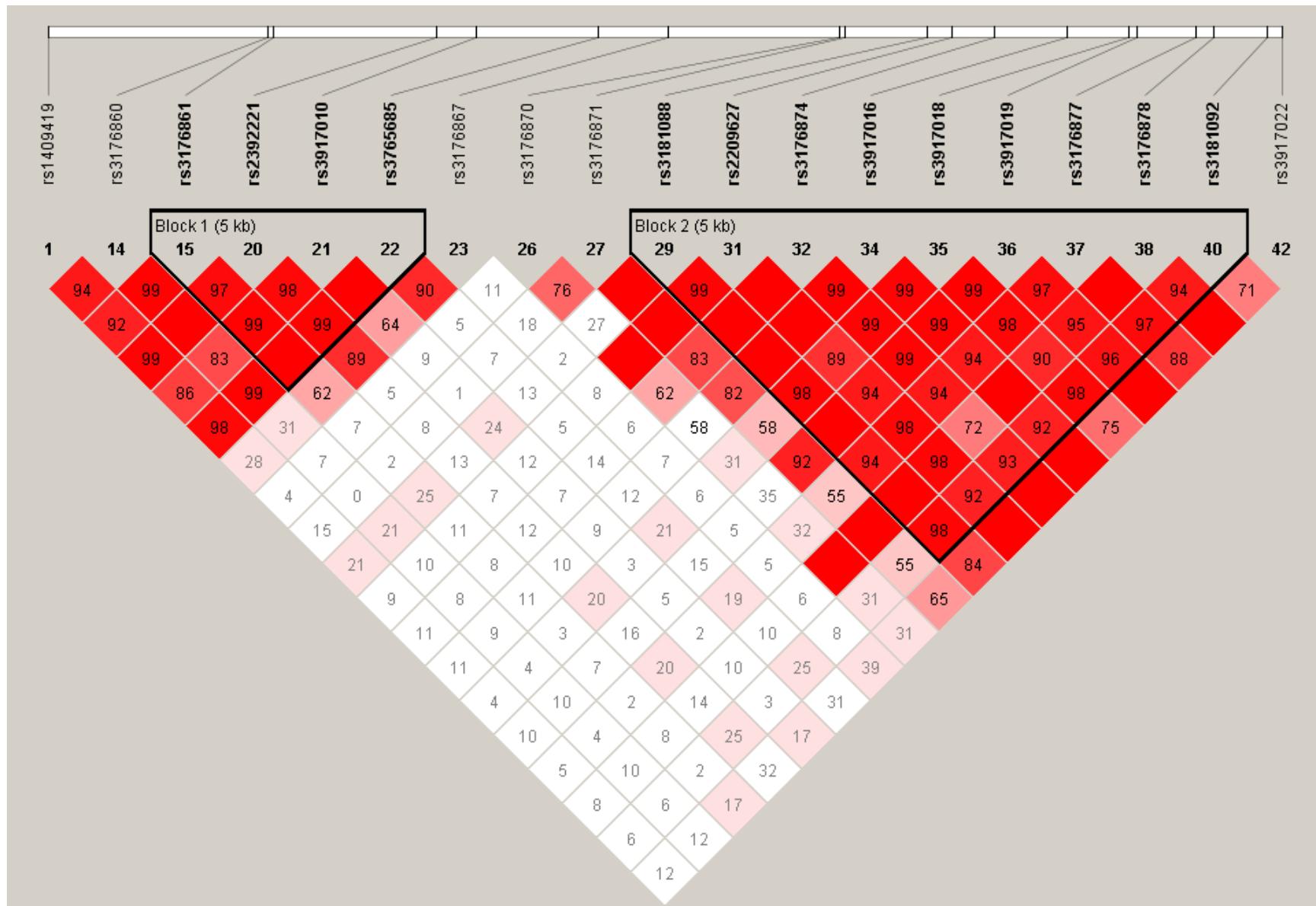
<sup>c</sup>FDR adjusted P values.



**Figure S1.** Flow chart of selection of incident CVD cases and the subcohort. Incident CVD cases include fatal and non-fatal CHD, stroke, and other CVD.



**Figure S2.** Linkage disequilibrium (LD) plot for *ICAM1* SNPs in Bangladeshi. The LD relationship between each pair of SNPs is indicated by the D prime, derived from the genotypes in the subcohort using the Haploview software. The shading indicates the extent of LD and a greater LD is represented by darker shading.



**Figure S3.** Linkage disequilibrium (LD) plot for *VCAM1* SNPs in Bangladeshi. The LD relationship between each pair of SNPs is indicated by the D prime, derived from the genotypes in the subcohort using the Haplovew software. The shading indicates the extent of LD and a greater LD is represented by darker shading.